

# SEQUENCE LISTING

<110> Duffy, Hao-Peng Xu  
 Shan, Ji-dong  
 Yuan, Li-ming  
 Dudman, Daniel  
 Calabro, Anthony

<120> Identification of Differentially Methylated  
 Multiple Drug Resistance Loci

<130> 52494/2202

<140> filed concurrently herewith

<141> 1999-11-08

<150> US 60/108,994

<151> 1998-11-08

<160> 46

<170> WordPerfect 8.0 for Windows

<210> 1

<211> 24

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<223> Synthetic adapter

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ctcgtcgtca ggtcagtgct tcac

24

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cggtgaagca ct

12

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tagagccacg tagctgctgt agtc

24

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cggactacag ca

12

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accgtggact ggatagggttc agac

24

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cgtctgaac ct

12

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<213> Homo sapiens  
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56

Met Ser Ala

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ggc gga gac ttc ggg aat ccg ctg agg aaa ttc aag ctg gtg ttc ctg 104  
Gly Gly Asp Phe Gly Asn Pro Leu Arg Lys Phe Lys Leu Val Phe Leu  
5 10 15

ggg gag caa agc gtt gca aag aca tct ttg atc acc aga ttc agg tat 152  
Gly Glu Gln Ser Val Ala Lys Thr Ser Leu Ile Thr Arg Phe Arg Tyr  
20 25 30 35

gac agt ttt gac aac acc tat cag gca ata att ggc att gac ttt tta 200  
Asp Ser Phe Asp Asn Thr Tyr Gln Ala Ile Ile Gly Ile Asp Phe Leu  
40 45 50

tca aaa act atg tac ttg gag gat gga aca atc ggg ctt cgg ctg tgg 248  
Ser Lys Thr Met Tyr Leu Glu Asp Gly Thr Ile Gly Leu Arg Leu Trp  
55 60 65

gat acg gcg ggt cag gaa cgt ctc cgt agc ctc att ccc agg tac atc 296  
Asp Thr Ala Gly Gln Glu Arg Leu Arg Ser Leu Ile Pro Arg Tyr Ile  
70 75 80

cgt gat tct gct gca gct gta gta gtt tac gat atc aca aat gtt aac 344  
Arg Asp Ser Ala Ala Ala Val Val Val Tyr Asp Ile Thr Asn Val Asn  
85 90 95

tca ttc cag caa act aca aag tgg att gat gat gtc aga aca gaa aga 392  
Ser Phe Gln Gln Thr Thr Lys Trp Ile Asp Asp Val Arg Thr Glu Arg  
100 105 110 115

gga agt gat gtt atc atc acg cta gta gga aat aga aca gat ctt gct 440  
Gly Ser Asp Val Ile Ile Thr Leu Val Gly Asn Arg Thr Asp Leu Ala  
120 125 130

gac aag agg caa gtg tca gtt gag gag gga gag agg aaa gcc aaa ggg 488  
Asp Lys Arg Gln Val Ser Val Glu Glu Gly Glu Arg Lys Ala Lys Gly  
135 140 145

ctg aat gtt acg ttt att gaa act agg gca aaa act gga tac aat gta 536  
Leu Asn Val Thr Phe Ile Glu Thr Arg Ala Lys Thr Gly Tyr Asn Val

150

155

160

aag cag ctc ttt cga cgt gta gca gca gct ttg ccg g  
 Lys Gln Leu Phe Arg Arg Val Ala Ala Ala Leu Pro

573

165

170

175

&lt;210&gt; 8

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic primer

&lt;400&gt; 8

tcctctagtt ccaccatgtc cac

23

&lt;210&gt; 9

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic primer

&lt;400&gt; 9

cacagccgaa gcccgattg

19

&lt;210&gt; 10

&lt;211&gt; 838

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 48..809

&lt;400&gt; 10

ccgggaggtc tctgggctga ggcggcgaca gctcctctag ttccacc atg tcc gcg  
 Met Ser Ala

56

1

ggc gga gac ttc ggg aat ccg ctg agg aaa ttc aag ctg gtg ttc ctg	104
Gly Gly Asp Phe Gly Asn Pro Leu Arg Lys Phe Lys Leu Val Phe Leu	
5 10 15	
ggg gag caa agc gtt gca aag aca tct ttg atc acc aga ttc agg tat	152
Gly Glu Gln Ser Val Ala Lys Thr Ser Leu Ile Thr Arg Phe Arg Tyr	
20 25 30 35	
gac agt ttt gac aac acc tat cag gca ata att ggc att gac ttt tta	200
Asp Ser Phe Asp Asn Thr Tyr Gln Ala Ile Ile Gly Ile Asp Phe Leu	
40 45 50	
tca aaa act atg tac ttg gag gat gga aca atc ggg ctt cgg ctg tgg	248
Ser Lys Thr Met Tyr Leu Glu Asp Gly Thr Ile Gly Leu Arg Leu Trp	
55 60 65	
gat acg gcg ggt cag gaa cgt ctc cgt agc ctc att ccc agg tac atc	296
Asp Thr Ala Gly Gln Glu Arg Leu Arg Ser Leu Ile Pro Arg Tyr Ile	
70 75 80	
cgt gat tct gct gca gct gta gta gtt tac gat atc aca aat gtt aac	344
Arg Asp Ser Ala Ala Ala Val Val Val Tyr Asp Ile Thr Asn Val Asn	
85 90 95	
tca ttc cag caa act aca aag tgg att gat gat gtc aga aca gaa aga	392
Ser Phe Gln Gln Thr Thr Lys Trp Ile Asp Asp Val Arg Thr Glu Arg	
100 105 110 115	
gga agt gat gtt atc atc acg cta gta gga aat aga aca gat ctt gct	440
Gly Ser Asp Val Ile Ile Thr Leu Val Gly Asn Arg Thr Asp Leu Ala	
120 125 130	
gac aag agg caa gtg tca gtt gag gag gga gag agg aaa gcc aaa ggg	488
Asp Lys Arg Gln Val Ser Val Glu Glu Gly Glu Arg Lys Ala Lys Gly	
135 140 145	
ctg aat gtt acg ttt att gaa act agg gca aaa act gga tac aat gta	536
Leu Asn Val Thr Phe Ile Glu Thr Arg Ala Lys Thr Gly Tyr Asn Val	
150 155 160	

aag cag ctc ttt cga cgt gta gca gca gct ttg ccg gga atg gaa agc 584  
 Lys Gln Leu Phe Arg Arg Val Ala Ala Ala Leu Pro Gly Met Glu Ser  
 165 170 175

aca cag gac gga agc aga gaa gac atg agt gac ata aaa ctg gaa aag 632  
 Thr Gln Asp Gly Ser Arg Glu Asp Met Ser Asp Ile Lys Leu Glu Lys  
 180 185 190 195

cct cag gag caa aca gtc agc gaa ggg ggt tgt tcc tgc tac tct ccc 680  
 Pro Gln Glu Gln Thr Val Ser Glu Gly Gly Cys Ser Cys Tyr Ser Pro  
 200 205 210

atg tca tct tca acc ctt cct cag aag ccc cct tac tct ttc att gac 728  
 Met Ser Ser Ser Thr Leu Pro Gln Lys Pro Pro Tyr Ser Phe Ile Asp  
 215 220 225

tgc agt gtg aat att ggc ttg aac ctt ttc cct tca tta ata acg ttt 776  
 Cys Ser Val Asn Ile Gly Leu Asn Leu Phe Pro Ser Leu Ile Thr Phe  
 230 235 240

tgc aat tca tca ttg ctg cct gtc tcg tgg aga tgatctatta gcttgacaag 829  
 Cys Asn Ser Ser Leu Leu Pro Val Ser Trp Arg  
 245 250 254

cacaaaaaa 838

<210> 11

<211> 762

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 1..762

<400> 11

atg tcc gcg ggc gga gac ttc ggg aat ccg ctg agg aaa ttc aag ctg 48  
 Met Ser Ala Gly Gly Asp Phe Gly Asn Pro Leu Arg Lys Phe Lys Leu  
 1 5 10 15

gtg ttc ctg ggg gag caa agc gtt gca aag aca tct ttg atc acc aga 96  
 Val Phe Leu Gly Glu Gln Ser Val Ala Lys Thr Ser Leu Ile Thr Arg

20

25

30

ttc agg tat gac agt ttt gac aac acc tat cag gca ata att ggc att 144  
 Phe Arg Tyr Asp Ser Phe Asp Asn Thr Tyr Gln Ala Ile Ile Gly Ile  
           35                          40                          45

gac ttt tta tca aaa act atg tac ttg gag gat gga aca atc ggg ctt 192  
 Asp Phe Leu Ser Lys Thr Met Tyr Leu Glu Asp Gly Thr Ile Gly Leu  
           50                          55                          60

cgg ctg tgg gat acg gcg ggt cag gaa cgt ctc cgt agc ctc att ccc 240  
 Arg Leu Trp Asp Thr Ala Gly Gln Glu Arg Leu Arg Ser Leu Ile Pro  
           65                          70                          75                          80

agg tac atc cgt gat tct gct gca gct gta gta gtt tac gat atc aca 288  
 Arg Tyr Ile Arg Asp Ser Ala Ala Ala Val Val Val Tyr Asp Ile Thr  
                                   85                                  90                                  95

aat gtt aac tca ttc cag caa act aca aag tgg att gat gat gtc aga 336  
 Asn Val Asn Ser Phe Gln Gln Thr Thr Lys Trp Ile Asp Asp Val Arg  
                                   100                                  105                                  110

aca gaa aga gga agt gat gtt atc atc acg cta gta gga aat aga aca 384  
 Thr Glu Arg Gly Ser Asp Val Ile Ile Thr Leu Val Gly Asn Arg Thr  
           115                          120                          125

gat ctt gct gac aag agg caa gtg tca gtt gag gag gga gag agg aaa 432  
 Asp Leu Ala Asp Lys Arg Gln Val Ser Val Glu Glu Gly Glu Arg Lys  
           130                          135                          140

gcc aaa ggg ctg aat gtt acg ttt att gaa act agg gca aaa act gga 480  
 Ala Lys Gly Leu Asn Val Thr Phe Ile Glu Thr Arg Ala Lys Thr Gly  
           145                          150                          155                          160

tac aat gta aag cag ctc ttt cga cgt gta gca gca gct ttg ccg gga 528  
 Tyr Asn Val Lys Gln Leu Phe Arg Arg Val Ala Ala Ala Leu Pro Gly  
                                   165                                  170                                  175

atg gaa agc aca cag gac gga agc aga gaa gac atg agt gac ata aaa 576  
 Met Glu Ser Thr Gln Asp Gly Ser Arg Glu Asp Met Ser Asp Ile Lys

180

185

190

ctg gaa aag cct cag gag caa aca gtc agc gaa ggg ggt tgt tcc tgc 624  
 Leu Glu Lys Pro Gln Glu Gln Thr Val Ser Glu Gly Gly Cys Ser Cys  
 195 200 205

tac tct ccc atg tca tct tca acc ctt cct cag aag ccc cct tac tct 672  
 Tyr Ser Pro Met Ser Ser Ser Thr Leu Pro Gln Lys Pro Pro Tyr Ser  
 210 215 220

ttc att gac tgc agt gtg aat att ggc ttg aac ctt ttc cct tca tta 720  
 Phe Ile Asp Cys Ser Val Asn Ile Gly Leu Asn Leu Phe Pro Ser Leu  
 225 230 235 240

ata acg ttt tgc aat tca tca ttg ctg cct gtc tcg tgg aga 762  
 Ile Thr Phe Cys Asn Ser Ser Leu Leu Pro Val Ser Trp Arg  
 245 250 254

<210> 12

<211> 254

<212> PRT

<213> Homo sapiens

<400> 12

Met Ser Ala Gly Gly Asp Phe Gly Asn Pro Leu Arg Lys Phe Lys Leu  
 1 5 10 15

Val Phe Leu Gly Glu Gln Ser Val Ala Lys Thr Ser Leu Ile Thr Arg  
 20 25 30

Phe Arg Tyr Asp Ser Phe Asp Asn Thr Tyr Gln Ala Ile Ile Gly Ile  
 35 40 45

Asp Phe Leu Ser Lys Thr Met Tyr Leu Glu Asp Gly Thr Ile Gly Leu  
 50 55 60

Arg Leu Trp Asp Thr Ala Gly Gln Glu Arg Leu Arg Ser Leu Ile Pro  
 65 70 75 80

Arg Tyr Ile Arg Asp Ser Ala Ala Ala Val Val Val Tyr Asp Ile Thr  
 85 90 95



Asn	Val	Asn	Ser	Phe	Gln	Gln	Thr	Thr	Lys	Trp	Ile	Asp	Asp	Val	Arg
			100						105					110	
Thr	Glu	Arg	Gly	Ser	Asp	Val	Ile	Ile	Thr	Leu	Val	Gly	Asn	Arg	Thr
			115						120					125	
Asp	Leu	Ala	Asp	Lys	Arg	Gln	Val	Ser	Val	Glu	Glu	Gly	Glu	Arg	Lys
			130						135					140	
Ala	Lys	Gly	Leu	Asn	Val	Thr	Phe	Ile	Glu	Thr	Arg	Ala	Lys	Thr	Gly
			145						150					155	
Tyr	Asn	Val	Lys	Gln	Leu	Phe	Arg	Arg	Val	Ala	Ala	Ala	Leu	Pro	Gly
									165					170	
Met	Glu	Ser	Thr	Gln	Asp	Gly	Ser	Arg	Glu	Asp	Met	Ser	Asp	Ile	Lys
									180					185	
Leu	Glu	Lys	Pro	Gln	Glu	Gln	Thr	Val	Ser	Glu	Gly	Gly	Cys	Ser	Cys
									195					200	
Tyr	Ser	Pro	Met	Ser	Ser	Ser	Thr	Leu	Pro	Gln	Lys	Pro	Pro	Tyr	Ser
									210					215	
Phe	Ile	Asp	Cys	Ser	Val	Asn	Ile	Gly	Leu	Asn	Leu	Phe	Pro	Ser	Leu
									225					230	
Ile	Thr	Phe	Cys	Asn	Ser	Ser	Leu	Leu	Pro	Val	Ser	Trp	Arg		
									245					250	

<210> 13

<211> 18

<212> DNA

<213> Homo sapiens

<400> 13

gga aca atc ggg ctt cgg

Gly Thr Ile Gly Leu Arg

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<211> 21

<212> DNA

<213> Homo sapiens

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21

Leu Arg Ser Leu Ile Pro Arg

1

5

<210> 15

<211> 39

<212> DNA

<213> Homo sapiens

<400> 15

ggg ctg aat gtt acg ttt att gaa act agg gca aaa act

39

Gly Leu Asn Val Thr Phe Ile Glu Thr Arg Ala Lys Thr

1

5

10

<210> 16

<211> 21

<212> DNA

<213> Homo sapiens

<400> 16

gga agc aga gaa gac atg agt

21

Gly Ser Arg Glu Asp Met Ser

1

5

<210> 17

<211> 15

<212> DNA

<213> Homo sapiens

<400> 17

gag caa aca gtc agc

15

Glu Gln Thr Val Ser

1

5

<210> 18

<211> 138

<212> DNA

<213> Homo sapiens

<400> 18

tac tct ccc atg tca tct tca acc ctt cct cag aag ccc cct tac tct 48  
Tyr Ser Pro Met Ser Ser Ser Thr Leu Pro Gln Lys Pro Pro Tyr Ser  
1 5 10 15

ttc att gac tgc agt gtg aat att ggc ttg aac ctt ttc cct tca tta 96  
Phe Ile Asp Cys Ser Val Asn Ile Gly Leu Asn Leu Phe Pro Ser Leu  
20 25 30

ata acg ttt tgc aat tca tca ttg ctg cct gtc tcg tgg aga 138  
Ile Thr Phe Cys Asn Ser Ser Leu Leu Pro Val Ser Trp Arg  
35 40 45

<210> 19

<211> 6

<212> PRT

<213> Homo sapiens

<400> 19

Gly Thr Ile Gly Leu Arg

1 5

<210> 20

<211> 7

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<400> 20

Leu Arg Ser Leu Ile Pro Arg

1 5

<210> 21

<211> 13

<212> PRT

<213> Homo sapiens

<400> 21

Gly Leu Asn Val Thr Phe Ile Glu Thr Arg Ala Lys Thr

1 5 10

<210> 22

<211> 7

<212> PRT

<213> Homo sapiens

<400> 22

Gly Ser Arg Glu Asp Met Ser

1

5

<210> 23

<211> 5

<212> PRT

<213> Homo sapiens

<400> 23

Glu Gln Thr Val Ser

1

5

<210> 24

<211> 46

<212> PRT

<213> Homo sapiens

<400> 24

Tyr Ser Pro Met Ser Ser Ser Thr Leu Pro Gln Lys Pro Pro Tyr Ser

1

5

10

15

Phe Ile Asp Cys Ser Val Asn Ile Gly Leu Asn Leu Phe Pro Ser Leu

20

25

30

Ile Thr Phe Cys Asn Ser Ser Leu Leu Pro Val Ser Trp Arg

35

40

45

<210> 25

<211> 1460

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 420..1043

<220>

<223> cDNA (composite of multiple cDNA clones)

<400> 25

gaattccggg cagctgtgga agctcaggcg ctgcgcgtga gaggtcccag atacgtctgc 60

ggttccgggt ccgccaccct cagcttctct tccccagggtc tgggagccga gtgcggaagg 120

agggaacggc cctagctttg ggaagccaga ggacaccctt ggctcctgcc gacaccgccc 180  
 tccttccctt cccagccgcg ggctcgcctc ggtgctaggc tactctgccg ggaggcggcg 240  
 gcggctgcca gtctgtggag agtcctgctg ccctccagcc gggctcctcc accgggcctt 300  
 gcagggggccg agagagctcg gtgcccgcctt ttccgctcgc ctttttcgctc agctggctgg 360  
 agcagcatcg gtccgggagg tctctaggct gaggcggcgg ccgctcctct agttccaca 419  
 atg tcc acg ggc gga gac ttc ggg aat ccg ctg agg aaa ttc aag ctg 467  
 Met Ser Thr Gly Gly Asp Phe Gly Asn Pro Leu Arg Lys Phe Lys Leu  
 1 5 10 15  
 gtg ttc ctg ggg gag caa agc gtt gga aag aca tct ttg atc acc aga 515  
 Val Phe Leu Gly Glu Gln Ser Val Gly Lys Thr Ser Leu Ile Thr Arg  
 20 25 30  
 ttc atg tat gac agt ttt gac aac acc tat cag gca aca att ggc att 563  
 Phe Met Tyr Asp Ser Phe Asp Asn Thr Tyr Gln Ala Thr Ile Gly Ile  
 35 40 45  
 gac ttt tta tca aaa act atg tac ttg gag gat cga aca atc agg ctt 611  
 Asp Phe Leu Ser Lys Thr Met Tyr Leu Glu Asp Arg Thr Ile Arg Leu  
 50 55 60  
 cag ctg tgg gat act gcg ggt cag gaa cgt ttc cgt agc ctc att ccc 659  
 Gln Leu Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Ser Leu Ile Pro  
 65 70 75 80  
 agt tac atc cgt gat tct gct gca gct gta gta gtt tac gat atc aca 707  
 Ser Tyr Ile Arg Asp Ser Ala Ala Ala Val Val Val Tyr Asp Ile Thr  
 85 90 95  
 aat gtt aac tca ttc cag caa act aca aag tgg att gat gat gtc aga 755  
 Asn Val Asn Ser Phe Gln Gln Thr Thr Lys Trp Ile Asp Asp Val Arg  
 100 105 110



<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 1..624

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<223> coding region of cDNA

<400> 26

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Met	Ser	Thr	Gly	Gly	Asp	Phe	Gly	Asn	Pro	Leu	Arg	Lys	Phe	Lys	Leu	
1				5					10					15		

gtg	ttc	ctg	ggg	gag	caa	agc	gtt	gga	aag	aca	tct	ttg	atc	acc	aga	96
Val	Phe	Leu	Gly	Glu	Gln	Ser	Val	Gly	Lys	Thr	Ser	Leu	Ile	Thr	Arg	
			20					25					30			

ttc	atg	tat	gac	agt	ttt	gac	aac	acc	tat	cag	gca	aca	att	ggc	att	144
Phe	Met	Tyr	Asp	Ser	Phe	Asp	Asn	Thr	Tyr	Gln	Ala	Thr	Ile	Gly	Ile	
		35					40					45				

gac	ttt	tta	tca	aaa	act	atg	tac	ttg	gag	gat	cga	aca	atc	agg	ctt	192
Asp	Phe	Leu	Ser	Lys	Thr	Met	Tyr	Leu	Glu	Asp	Arg	Thr	Ile	Arg	Leu	
	50					55				60						

cag	ctg	tgg	gat	act	gcg	ggt	cag	gaa	cgt	ttc	cgt	agc	ctc	att	ccc	240
Gln	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Arg	Phe	Arg	Ser	Leu	Ile	Pro	
65					70				75					80		

agt	tac	atc	cgt	gat	tct	gct	gca	gct	gta	gta	gtt	tac	gat	atc	aca	288
Ser	Tyr	Ile	Arg	Asp	Ser	Ala	Ala	Ala	Val	Val	Val	Tyr	Asp	Ile	Thr	
					85				90					95		

aat	gtt	aac	tca	ttc	cag	caa	act	aca	aag	tgg	att	gat	gat	gtc	aga	336
Asn	Val	Asn	Ser	Phe	Gln	Gln	Thr	Thr	Lys	Trp	Ile	Asp	Asp	Val	Arg	
			100				105					110				

aca	gaa	aga	gga	agt	gat	gtt	atc	atc	atg	cta	gta	gga	aat	aaa	aca	384
Thr	Glu	Arg	Gly	Ser	Asp	Val	Ile	Ile	Met	Leu	Val	Gly	Asn	Lys	Thr	
	115						120				125					

gat ctt gct gac aag agg caa gtg tca att gag gag gga gag agg aaa 432  
 Asp Leu Ala Asp Lys Arg Gln Val Ser Ile Glu Glu Gly Glu Arg Lys  
 130 135 140

gcc aaa gag ctg aat gtt atg ttt att gaa act agt gca aaa gct gga 480  
 Ala Lys Glu Leu Asn Val Met Phe Ile Glu Thr Ser Ala Lys Ala Gly  
 145 150 155 160

tac aat gta aag cag ctc ttt cga cgt gta gca gca gct ttg ccg gga 528  
 Tyr Asn Val Lys Gln Leu Phe Arg Arg Val Ala Ala Ala Leu Pro Gly  
 165 170 175

atg gaa agc aca cag gac aga agc aga gaa gat atg att gac ata aaa 576  
 Met Glu Ser Thr Gln Asp Arg Ser Arg Glu Asp Met Ile Asp Ile Lys  
 180 185 190

ctg gaa aag cct cag gag caa cca gtc agt gaa gga ggc tgt tcc tgc 624  
 Leu Glu Lys Pro Gln Glu Gln Pro Val Ser Glu Gly Gly Cys Ser Cys  
 195 200 205

<210> 27

<211> 208

<212> PRT

<213> Homo sapiens

<400> 27

Met Ser Thr Gly Gly Asp Phe Gly Asn Pro Leu Arg Lys Phe Lys Leu  
 1 5 10 15

Val Phe Leu Gly Glu Gln Ser Val Gly Lys Thr Ser Leu Ile Thr Arg  
 20 25 30

Phe Met Tyr Asp Ser Phe Asp Asn Thr Tyr Gln Ala Thr Ile Gly Ile  
 35 40 45

Asp Phe Leu Ser Lys Thr Met Tyr Leu Glu Asp Arg Thr Ile Arg Leu  
 50 55 60

Gln Leu Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Ser Leu Ile Pro  
 65 70 75 80



Ser Tyr Ile Arg Asp Ser Ala Ala Ala Val Val Val Tyr Asp Ile Thr  
 85 90 95  
 Asn Val Asn Ser Phe Gln Gln Thr Thr Lys Trp Ile Asp Asp Val Arg  
 100 105 110  
 Thr Glu Arg Gly Ser Asp Val Ile Ile Met Leu Val Gly Asn Lys Thr  
 115 120 125  
 Asp Leu Ala Asp Lys Arg Gln Val Ser Ile Glu Glu Gly Glu Arg Lys  
 130 135 140  
 Ala Lys Glu Leu Asn Val Met Phe Ile Glu Thr Ser Ala Lys Ala Gly  
 145 150 155 160  
 Tyr Asn Val Lys Gln Leu Phe Arg Arg Val Ala Ala Ala Leu Pro Gly  
 165 170 175  
 Met Glu Ser Thr Gln Asp Arg Ser Arg Glu Asp Met Ile Asp Ile Lys  
 180 185 190  
 Leu Glu Lys Pro Gln Glu Gln Pro Val Ser Glu Gly Gly Cys Ser Cys  
 195 200 205

<210> 28  
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 tcctctagtt ccaccatgtc cgc

23

<210> 29  
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gtaaaacgac ggccagt

17

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<400> 30

agcggataac aatttcacac agga

24

<210> 31

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 31

tcctctagtt ccacaatgtc c

21

<210> 32

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

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